

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 16, 2003, 10:39:12, Search time: 7.28771 seconds
(without alignments)
28.464 Million cell updates/sec

Title: US-09-856-070-25

Perfect score: 23
Sequence: 1 MLRLQ 5

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	100.0	160	Y650_TREPA	G83656 treponema p
2	23	100.0	196	RL19_HUMAN	P14118 homo sapien
3	23	100.0	244	UL51_USVE4	G69638 equine herp
4	23	100.0	245	UL51_USVEB	P28961 equine herp
5	23	100.0	288	P8P1_SCHPO	G74456 schizosacch
6	23	100.0	313	PYRH_AGR06	G8u79 agrobacteri
7	23	100.0	313	PYRH_RHIME	Q52q15 rhizobium m
8	23	100.0	317	MTB1_NEIGO	Q52603 nelisseria g
9	23	100.0	318	MTB2_HAEAE	Q30868 haemophilus
10	23	100.0	322	PYRH_BRIME	G8y662 brucella me
11	23	100.0	322	PYRH_XYLFA	G9p668 xylicella fas
12	23	100.0	323	PYRH_RALSO	G8y112 ralstonia s
13	23	100.0	326	PYRH_RH110	G98m86 rhizobium l
14	23	100.0	332	PYRH_CAF0P	G9a1k4 caulobacter
15	23	100.0	334	PYRH_PSEAE	Q59653 pseudomonas
16	23	100.0	334	PYRH_PSEPU	Q59711 pseudomonas
17	23	100.0	383	VJIM_ECOLI	P39384 escherichia
18	23	100.0	423	FLGH_HRLMU	P58611 heliobacter
19	23	100.0	503	PUR1_PASMU	G916b8 pasteurella
20	23	100.0	504	PUR1_HAEIN	P43854 haemophilus
21	23	100.0	580	E2R1_BGVIN	P31576 bos taurus
22	23	100.0	586	E2R1_HUMAN	F15911 homo sapien
23	23	100.0	586	P2R1_MOUSE	P26040 mus musculu
24	23	100.0	670	YQ66_CAFU1	G20466 caenorhabdi
25	21	91.3	269	N0DC_VIRCH	G9kv27 vibrio chol
26	21	91.3	289	LEF4_PSEST	G2e1c6 pseudomonas
27	21	91.3	366	ODPB_SCHFO	Q09171 schizosacch
28	21	91.3	396	G4SA_DROME	G9v6a9 drosophila
29	21	91.3	397	GAL1_TREPA	G83433 treponema p
30	21	91.3	429	PUR2_VIRCH	G9A981 vibrio chol
31	21	91.3	437	PUR2_XYLFA	G9p609 xylicella fas
32	21	91.3	459	YGM9_YEAST	F53083 saccharomyc
33	21	91.3	461	G6PT_PTIME	G92362 rhizobium m

RESULT 1

Y650_TREPA
ID Y650_TREPA STANDARD: PRT: 160 AA.
AC G83656;
DI 30-MAY-2000 (Rel. 39, Created)
DI 30-MAY-2000 (Rel. 39, Last sequence update)
EI 18-JUL-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0650.
GN TP0650.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NC NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Nichols;
FX FRASER-98442770: PubMed-9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White G., Sutton G.G., Dodson R., Gwinn M., Hickey K.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Uitterback T., McDonald L., Attiachi P., Bowman G., Cotton M.B., Fujii C., Garland S., Hatch H., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.G., Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis spirochete";
RL Science 281:375-388(1998).
CC - SIMILARITY: BELONGS TO THE UPF0054 FAMILY.
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CC EMBL: AF061239, AAC56523.1;
CC TIGR: TP0650;
CC InterPro: IP0002036; UPF0054.
CC Pfam: PF02130; UPF0054; 1.
CC Prodom: P005644; UPF0054; 1.
CC TIGRfams: TIGR00043; UPF0054; 1.
CC PROSITE: PS01356; GPF0024; 1.
CC KW Hypothetical protein, Complete proteome.
SQ SEQUENCE 160 AA; 18612 MW; 654796A81A7L898F CRC64;

Query Match: 100.0%, Score 23; DB 1; Length 160;
Best local Similarity 100.0%; Prod. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLRLQ 5
Db 137 MLRLQ 141

RESULT 2

RL19_HUMAN
ID RL19_HUMAN STANDARD; PRI; 196 AA.
AC P14118; P22908;
DT 01-JAN-1990 (Rel. 13, Created)
DI 01-JAN-1990 (Rel. 13, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L19.
GN RL19.
OS Homo sapiens (human).
OS Mus musculus (mouse).
OS Rattus norvegicus (rat).
CA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CA Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-92285147; PubMed-1598220;
RA Kumabe T., Schma Y., Yamamoto I.;
RI "Human cDNAs encoding elongation factor 1 gamma and the ribosomal protein L19.";
RL Nucleic Acids Res. 20:2598-2598(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-93185086; PubMed-8095182;
RA Henry J.L., Coquin D.L., King C.R.;
RI "High level expression of the ribosomal protein L19 in human breast tumors that overexpress erbB-2.";
RL Cancer Res. 53:1403-1408(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-Human;
RX MEDLINE-91090840; PubMed-1702292;
RA Nakamura T., Ono M., Mariage-Samson P., Hillova T., Hill M.;
RI "Nucleotide sequence of mouse L19 ribosomal protein cDNA isolated in screening with the oncogene probes.";
RL DNA Cell Biol. 9:697-703(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa K., Izawa M., Nishi F., Iiyosawa H., Kondo S., Yamazaki T., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H., Kachi P., Lewis S., Matsuo Y., Nikita T., Iwano S., Gotohori T., Sakai K., Okido T., Furuno M., Aono H., Haidarelli R., Barsh G., Blake J., Bollati D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Holman M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring H., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Scheenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Waki K.H., Weitz C., Whitaker C., Wilming L., Wushaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
RI "Functional annotation of a full length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES-Mouse;
RA Strausberg R.;
RI Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [7]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC SPECIES-Rat;
RX MEDLINE-87109220; PubMed-3542997;
RA Chan Y.-L., Lin A., McNally J., Peleg D., Meyuhas O., Wool I.G.;
RI "The primary structure of rat ribosomal protein L19. A determination from the sequence of nucleotides in a cDNA and from the sequence of amino acids in the protein.";
RL J. Biol. Chem. 262:1111-1115(1987).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES-Rat; STRAIN-Fischer;
RX MEDLINE-95309903; PubMed-7789470;
RA Davies R., Fried M.;
RI "The L19 ribosomal protein gene (Rpl19): gene organization, chromosomal mapping, and novel promoter region.";
RL Genomics 25:372-380(1995).
RN [9]
RP SIMILARITY BELONGS TO THE L19F FAMILY OF RIBOSOMAL PROTEINS.
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CC EMBL: X63527; CAA45090.1;
DR EMBL: X63527; CAA45090.1;
DR EMBL: S56985; AAB25672.1;
DR EMBL: BC000530; AAB00530.1;
DR EMBL: BC013016; AAB13016.1;
DR EMBL: M62952; AAB48630.1;
DR EMBL: AK010440; AAB26941.1;
DR EMBL: BC010710; AAB10710.1;
DR EMBL: J02650; AAB42071.1;
DR EMBL: X82202; CAA57685.1;
DR PIR: S09560; K5RT19.
DR PIR: A36554; A36554.
DR PIR: S22656; S22656.
DR PIR: A48992; A48992.
DR Genew: HGNC:10312; RPL19.
DR MIM: 180456;
DR MGI: 98020; Rpl19.
DR InterPro: IPR000196; Ribosomal_L19c.
DR Pfam: PF01280; Ribosomal_L19c; 1.
DR PROSITE: PS00526; RIBOSOMAL_L19c; 1.
FW Ribosomal protein.
FT CONFLICT 179 179 A -> S (IN REF. 4).
SQ SEQUENCE 196 AA; 23466 MW; 4AF506393F52216 CRC64;
Query Match 100.0%; Score 23; DH 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MURIO 5
DB 3 MURIO 7
RESULT 3
U151_HSVF4
ID U151_HSVF4 STANDARD; PRI; 241 AA.
AC Q00018;
DI 01-DEC-1992 (Rel. 24, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DI 01-DEC-1992 (Rel. 24, Last annotation update)
DE Gene 8 protein.
GN 8 OR B2
OS Equine herpesvirus type 4 (strain 1942) (EHV 4) (equine herpesvirus type 1 subtype 2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10333;
RN [1]

SEQUENCE FROM N.A.
 MEDLINE-91202570; PubMed-1850013;
 Whitaker G.R., Raggio M.P., Halliburton L.W., Killington R.A.,
 Allen G.P., Meredith D.M.;
 "Antigenic and protein sequence homology between V33/14, a herpes
 simplex virus type 1 tegument protein, and gp10, a glycoprotein of
 equine herpesvirus 1 and 4";
 J. Virol. 65:2420-2426(1991);
 CC -/- SIMILARITY: RELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 0151;
 CC BHV-1 8, AND VZV 7;
 CC
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 CC
 CC EMBL: X17684; CAA35668.1;
 CC PIR: S36703; S36703;
 CC SEQUENCE: 241 AA; 26238 MW; 3F309FA3:MHQPP Q8261;
 Query Match 100.0%, Score 23, DB 1, Length 244,
 Best Local Similarity 100.0%, Pred No. 20;
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 Oy 1 MLRQ 5
 Db 34 MLRQ 38
 |||||
 RESULT 4
 UL51_HSVB STANDARD; PROT; 245 AA;
 AC P28961;
 DT 01-DEC-1992 (Pel. 24, Created)
 DT 01-DEC-1992 (Pel. 24, Last sequence update)
 DI 01-DEC-1992 (Pel. 24, Last annotation update)
 DE Gene 8 protein.
 GN 8.
 OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1)
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Alphaherpesvirinae; Varicellovirus
 CC NCHL_faxid-31520;
 CC
 CC SEQUENCE FROM N.A.
 CC MEDLINE-92295566; PubMed-118606;
 CC Telford E.A.R., Watson M.S., McBride K., Davidson A.;
 RT "The DNA sequence of equine herpesvirus-1";
 RL Virology 189:304-316(1992)
 CC -/- SIMILARITY: RELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 0151;
 CC BHV-1 8, AND VZV 7;
 CC
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 CC
 CC EMBL: M86664; AAR02443.1;
 CC PIR: I36795; W/HEA7; 26365 MW; 205F004A80242A5 Q8264;
 CC SEQUENCE: 245 AA; 26365 MW;
 Query Match 100.0%, Score 23, DB 1, Length 245,
 Best Local Similarity 100.0%, Pred. No. 21;
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 Oy 1 MLRQ 5
 Db 33 MLRQ 37
 |||||

RESULT 5
 PEPL_SCHPO STANDARD; PROT; 288 AA;
 AC G74456;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sorine/threonine protein kinase pepl (EC 2.7.1.37) (Cyclin-dependent
 DE kinase pepl) (PH085 homolog).
 GN PEPL-04-SP01004.11.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetaceae; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes;
 CC NCHL_faxid-4890;
 CC
 CC SEQUENCE FROM N.A.
 CC STRAIN 972;
 CC MEDLINE-20437747; PubMed-10982385;
 CC Tanaka K., Okajima H.;
 CC "A cyclin-like cyclin activates the Wee2p-Cdc10p cell cycle 'start'
 CC transcriptional factor complex in fission yeast";
 CC Mol. Biol. Cell 11:2845-2862(2000).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN-972;
 CC MEDLINE-21848401; PubMed-11859360;
 CC Wood V., Gwilliam P., Palandream M.A., Lyne M., Lyne P., Stewart A.,
 CC Squires J., Pear N., Hayles T., Baker S., Basham D., Bowman S.,
 CC Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 CC Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 CC Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,
 CC Holroyd S., Horsey T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
 CC James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 CC Moore F., Mouton R., Mudd J., Murphy L., Niblett D., Odell C.,
 CC Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 CC Rutherford K., Rutter S., Saunders D., Sanger K., Sharp S.,
 CC Skelton J., Simmonds M., Squires P., Squares S., Stevens K.,
 CC Taylor K., Taylor R.G., Tivoy A., Walsh S.V., Warren T., Whitehead S.,
 CC Woodward J., Velekaert G., Aert P., P-ken T., Grymberg B.,
 CC Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 CC Gabel C., Fuchs M., Frilze G., Holzer E., Moestl D., Hilbert R.,
 CC Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 CC Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle H.,
 CC Goffeau A., Cadieu E., Dreano S., Gloux S., Leliane V., Mottier S.,
 CC Galibert F., Aves S., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 CC Lucas M., Karpel M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 CC Daga P.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,
 CC Camigao A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 CC Corradi F., Lowe T., McCombie W.P., Paulsen O., Petashkin J.,
 CC Supakowski G.V., Ussery D., Harrell B.G., Nurse P.;
 CC "The genome sequence of Schizosaccharomyces pombe";
 CC Nature 415:871-882(2002).
 CC -/- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -/- SUBUNIT: Interacts with the past cyclin.
 CC -/- SIMILARITY: RELONGS TO THE SHK/INK FAMILY OF PROTEIN KINASES.
 CC CDC2/COKX SUBFAMILY.
 CC
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 CC
 CC EMBL: A031535; CAA20750.1;
 CC EMBL: A045127; AAR16402.1;
 CC HSPB; P24941; 1CKP.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.

Query Match 100.0%; Score 23; pH 1; Length 413;
Best local Similarity 100.0%; pred. No. 27;

RA Basoltero, R., Kyriakides N., Overbeck R.
 RT "The genome sequence of the facultative intracellular pathogen
 KL *Bruceella melitensis*."
 Proc. Natl. Acad. Sci. U.S.A. 99:444-448(2002)
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 CC
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 CC
 DR EMBL: A009702; AAL5912.1;
 DR InterPro: IPR002029; Asp/orn_Corranf
 DR InterPro: IPR002082; Asp_carmiltransf.
 DR Pfam: PF00185; OTCace; 1.
 DR Pfam: PF02729; OTCace_N; 1.
 DR PRINTS: PR01000; AOTCASE
 DR TIGRFS: TIGR00670; asp_cab.tr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
 KW Pyrimidine biosynthesis, Transferease, Complete proteome.
 SQ SEQUENCE 322 AA; 34892 MW; 8184298851B9521B CRC64.
 Query Match 100.0%; Score 23; DR 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLQ 5
 DB 228 MRLQ 232
 RESULT 11
 PYRB_XYLEA STANTAPP: PPT: 322 AA.
 ID PYRB_XYLEA
 AC QYRB68;
 DT 15 JUN-2002 (Rel. 41, Created)
 DT 15 JUN-2002 (Rel. 41, Last sequence update)
 DT 15 JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE Transcarbamylase) (ATCase).
 GN PYRB OR XF2226.
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OC NCBI_TaxID=2371;
 RP SEQUENCE FROM N.A.
 RC STRAIN 9456;
 RX MEDLINE:20465717; PubMed:10910447;
 RA Simpson A.J.G., Reznach F.C., Artuda P., Abreu F.A., Aceneto M.,
 RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Porcio S., Rove J.M., Briones M.R.S.,
 RA Bento M.R.P., Canagao A.A., Canagao L.E.A., Carraro D.M., Carter H.,
 RA Colauto N.H., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorty H.,
 RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Frana J.S., Franca S.G., Franco M.C., Frohme M., Furlan L.R.,
 RA Gardner M., Goldman G.H., Goldman M.H.S., Gomes S.T., Gruber A.,
 RA Ho P.L., Holsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramao E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.H.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.P., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,

RA Peixoto R.R., Pereira G.A.G., Pereira H.A. Jr., Pasquero J.H.,
 RA Quaggio R.B., Roberto P.C., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.F., da Silva A.M., da Silva F.E., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siguelia W.J., de Souza A.A.,
 RA de Souza A.P., Torenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*."
 RL Nature 406:151-159(2000).
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -!- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -!- SUBUNIT: CONTAINS SIX CATALYTIC AND SIX REGULATORY CHAINS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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 CC
 DR EMBL: A004045; AAF85025.1;
 DR HSSE, P00479; 3CSU.
 DR InterPro: IPR002029; Asp/orn_Corranf.
 DR InterPro: IPR002082; Asp_carmiltransf.
 DR TIGRFS: TIGR00185; OTCace; 1.
 DR Pfam: PF00185; OTCace; 1.
 DR Pfam: PF02729; OTCace_N; 1.
 DR PRINTS: PR01000; AOTCASE.
 DR TIGRFS: TIGR00670; asp_cab.tr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
 KW Pyrimidine biosynthesis, Transferease, Complete proteome.
 SQ SEQUENCE 322 AA; 34637 MW; 01005C24F5A7EAD CRC64;
 Query Match 100.0%; Score 23; DR 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLQ 5
 DB 237 MRLQ 241
 RESULT 12
 PYRB_RALSO STANDARD: PPT: 323 AA.
 ID PYRB_RALSO
 AC Q8Y112;
 DT 15 JUN-2002 (Rel. 41, Created)
 DT 15 JUN-2002 (Rel. 41, Last sequence update)
 DT 15 JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE Transcarbamylase) (ATCase).
 GN PYRB OR RSC0578 OR RSC0583.
 OS *Ralstonia solanacearum* (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria, beta subdivision; Ralstonia group;
 OC Ralstonia.
 OC NCBI_TaxID=305;
 RP SEQUENCE FROM N.A.
 RC STRAIN-GM1000;
 RX MEDLINE:21681879; PubMed:11823852;
 RA Salanoubat M., Genin S., Arliquene F., Gouzy J., Manqueot S.,
 RA Ariat M., Billault A., Brotter P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Claude J., Reard C., Cunha S., Demange N.,
 RA Caspin C., Lavoie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Thebaud P., Whalen M., Winkler P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate - phosphate

CC N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 CC
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 CC
 DR EMBL: AL646060; CAU14208.1; .
 DR InterPro: IPR002029; Asp_gln_cotranf.
 DR Pfam: PF00185; OTCase_N; 1.
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_cablr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 323 AA: 35133 MW: 17060440320T2 CR664.

 Query Match 100.0%; Score 23; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLQ 5
 DB 237 MRLQ 241

 RESULT 13
 PYRB_RHIL0
 ID PYRB_RHIL0 STANDARD: PPT: 326 AA.
 AC Q98M86;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE transcarbamylase) (ATCase).
 GN PYRB OR MR0686.
 GS Rhizobium loti (Mesorhizobium loti)
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Phyllobacteriaceae; Mesorhizobium
 CC NCBI_TaxID=381;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MAFF303099;
 RC MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Yano T., Sakamoto S.,
 RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsushima M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Takata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti".
 RL DNA Res. 7:331-338(2000).
 CC
 CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate -> phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 CC
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 CC
 DR EMBL: AP002995; BAB16227.1; .
 DR InterPro: IPR002029; Asp_gln_cotranf

DR InterPro: IPR002082; Asp_cabmltransf.
 DR Pfam: PF00185; OTCase_N; 1.
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_cablr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 326 AA: 35212 MW: 17566140593T25 CR664.

 Query Match 100.0%; Score 23; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRLQ 5
 DB 228 MRLQ 232

 RESULT 14
 PYRB_CAUCR
 ID PYRB_CAUCR STANDARD: PPT: 332 AA.
 AC Q9A5K4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
 DE transcarbamylase) (ATCase).
 GN PYRB OR G2443.
 GS Caulobacter crescentus.
 CC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 CC Caulobacter;
 CC NCBI_TaxID=155892;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=ATCC 19089 / CB15;
 RC MEDLINE=21173698; PubMed=11259647;
 RA Nieman W.C., Feldblyum T.V., Laub M.T., Paulsen O., Nelson K.E.,
 RA Eisen J., Heidelberg J.P., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Gray M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Krumholz M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro B., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus".
 RL F1000 Natl. Acad. Sci. U.S.A. 98:436-443(2001).
 CC
 CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate -> phosphate
 CC + N-carbamoyl-L-aspartate.
 CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
 CC -1- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 CC
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 CC
 DR EMBL: AE005913; MAK24414.1; .
 DR HSSP: P00479; ACSU.
 DR TIGRfams: TIGR02443; .
 DR InterPro: IPR002029; Asp_gln_cotranf.
 DR InterPro: IPR002082; Asp_cabmltransf.
 DR Pfam: PF00185; OTCase_N; 1.
 DR PRINTS: PR00100; AOTCASE.
 DR TIGRfams: TIGR00670; asp_cablr; 1.
 DR PROSITE: PS00097; CARBAMOYLTRANSFERSH; 1.
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 332 AA: 35509 MW: 132610050131AE4 CR664.

 Query Match 100.0%; Score 23; DB 1; Length 332;
 Best Local Similarity 100.0%; Pred. No. 29;

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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
QY      1 MLRLQ 5
      11111
Db      237 MLRLQ 241

Search completed: January 16, 2003, 16:51:16
Job time . 9.28571 secs

RESULTS 15
PYRB_PSEAF
ID PYRB_PSEAF STANDARD: PRT: 334 AA.
AC Q59653;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.1.3.2) (Aspartate
DE transcarbamylase) (ATCase).
GN PYRB OR PA0402.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
CX NCBI_TaxID=287;
LN [1]
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 15692 / PA01;
RA Vickrey J.F., Schurr M.J., Benjamin R.C., Chin R., Shantley M.S.,
RA O'Donovan G.A.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
LN [2]
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q., Erwin A.L., Mizuuchi S.D., Warrenner P.,
RA Blekey M.J., Brinkman F.S.L., Hutnagle W.G., Kowalik D.J., Lagrou M.,
RA Garber R.L., Gentry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.P., Kas A., Jarbq K., Lim P.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Keizer J., Sator M.H., Hancock R.P.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RA opportunistic pathogen."
RL Nature 406:959-964 (2000).
CC -1 CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate -> phosphate
CC + N-carbamoyl-L-aspartate.
CC -1 PATHWAY: pyrimidine biosynthesis; second step.
CC -1 SUBUNIT: HETERODIMER OF 6 ACTIVE PYRB SUBUNITS AND 6 NON-
CC CATALYTIC PYRB SUBUNITS (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO THE ATCASES/UTCASES FAMILY.
CC -----
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CC -----
DR EMBL: L19649; AAA5976.1; -
DR EMBL: AE004477; BAG03791.1; -
DR USSP: P00479; 3CS0.
DR InterPro: IPR002029; Asp/arg_Glnanti.
DR InterPro: IPR002082; Asp_carbamyltransf.
DR Pfam: PF00185; OTCace; 1.
DR Pfam: PF02729; OTCace_N; 1.
DR PRINTS: PR00100; AOTCASE.
DR TIGRfam: TIGR00670; asp_carb_lir; 1.
DR PROSITE: PS00097; CARBAMOYLTRANSFERASE; 1.
KW Pyrimidine biosynthesis; Transferase; Complete proteome.
FT CONFLICT 206 206 R -> A (IN REF. 1).
SQ SEQUENCE 334 AA; 36629 MW; 2DC90450FA2442E9 CRC64;

Query Match      100.0%      Score 23; DB 1; Length 334;
Best Local Similarity 100.0%; Pred. No. 29;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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